

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.

Application Serial Number: US/09/676,249D
Source: IFW/6
Date Processed by STIC: 10-26-04

ENTERED



IFW16

RAW SEQUENCE LISTING

DATE: 10/26/2004

PATENT APPLICATION: US/09/676,249D

TIME: 16:00:00

Input Set : A:\3153.162.PC10555A.Second.Substitute.Seq.10.19.04.ST25.txt

Output Set : N:\CRF4\10262004\I676249D.raw

3 <110> APPLICANT: Pfizer, Inc. and Pfizer Products, Inc.
 5 <120> TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS OF THE MYCOPLASMA HYOPNEUMONIAE

mhp3

6 GENE AND USES THEREOF

8 <130> FILE REFERENCE: 3153.00162/PC10555

10 <140> CURRENT APPLICATION NUMBER: US 09/676,249D

11 <141> CURRENT FILING DATE: 2000-09-29

13 <150> PRIOR APPLICATION NUMBER: US Prov. 60/156,602

14 <151> PRIOR FILING DATE: 1999-09-29

16 <160> NUMBER OF SEQ ID NOS: 42

18 <170> SOFTWARE: PatentIn version 3.2

20 <210> SEQ ID NO: 1

21 <211> LENGTH: 1692

22 <212> TYPE: DNA

23 <213> ORGANISM: Mycoplasma hyopneumoniae

25 <400> SEQUENCE: 1

26 gtttttgaat ataatagaaa atgtaaaata aaaattaatt tattaaaaaa taattgaaag 60
 28 tcacgtaaat taaaacaatt aattaggaga acaactatga aaaaaaagat aaaatgaaat 120
 30 aaatttcttg gcttaggctt agtttttccg ctttcagcaa tcgcgacaat ctctgccgga 180
 32 tgttgggata aagaaacaac taaagaagaa aaatcagccg ataatacaaaa taagcaaatc 240
 34 actgatgtct caaaaatttc aggactagtt aatgaacgaa aatccgaaat tatggccgca 300
 36 aaagctgatg caaacaaaca ttttgggcta aatatggcaa ttgtaaccgc tgggtggaacg 360
 38 gtaaatgata attcatttaa ccaatcaagt tgagaggcaa ttcaacaact tggcgctctt 420
 40 actggagggtg agattacttc agtagatagt tcaactgctg aacttgaagg aaaatatagc 480
 42 tcacttgcta ataccaacaa aaatgtttga gtactttctg gttttcaaca cgggtgatgcg 540
 44 ttcacaagat gattaaaaat ccctgaaaat aagcaattat ttactgaaaa aaatattatc 600
 46 atactcggaa ttgactgaac tgatactgaa aatgtaattc caacaggctc atataattaat 660
 48 ttaacctata aaactgaaga agccggatga cttgcaggat atgcgaatgc ttcccttttg 720
 50 gcaaaaaaat tcccaagtga tccaactaaa agatcagcaa ttgttatcgg tgggtgggatt 780
 52 tcgccagctg taactgattt tatcgctggg tatctagccg gaattaaagc ttgaaatcta 840
 54 aaaaattctg ataaaaaac aaagataaca actgataaaa tcgagataaa tcttgggttt 900
 56 gatgttcaag atacttcaac aaaagaaaga cttgaacaaa ttgcttcaaa agataaacct 960
 58 tcaacactat tagctgtcgc tggaccactt actgaaattt tctcggatat aatcgcaaac 1020
 60 caaatgatc gttatctcat tgggtgttgac accgaccaat cacttgttta taaaaaact 1080
 62 aaaaataaat ttttcacctc aattttgaaa aatttaggtt actccgtttt cagcgttctt 1140
 64 agtgatttat ataccaaaaa atcaaattca agaaatttag cgggctttga atttggtaaa 1200
 66 aaaagtgcaa ccgtttatct tggaattaaa gacaggtttg tcgatattgc tgatacttct 1260
 68 ttagaaggca atgataaaaa actcgcaact gaagccattt ctgaagctaa aaaagaattt 1320
 70 gaagaaaaaa ctaagacaat tcctgccgaa gaagtctgta aaactttaga aattccggaa 1380
 72 atgcctgata aacaacctga taagcaacag gaaagcttag acaaactaat taccgatatt 1440
 74 aataaaaaat aagtaagaaa aaataacaat tttttaacat tatacttttt tttagagatt 1500
 76 aattttcttc taatttagtt taatttaata taaaattata ttaaattaaa aaaataaaaa 1560
 78 atccggacta tttttgttcc ggatttttta tttttgtgtt actatttaat ataataataa 1620
 80 atcaggatta tgcaattgaa tttattcaag tctcgaaaaa atttggcagt ttttatgcca 1680

(pg. 6)

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85 <210> SEQ ID NO: 2
86 <211> LENGTH: 451
87 <212> TYPE: PRT
88 <213> ORGANISM: Mycoplasma hyopneumoniae
90 <400> SEQUENCE: 2
92 Met Lys Lys Lys Ile Lys Trp Asn Lys Phe Leu Gly Leu Gly Leu Val
93 1          5          10          15
96 Phe Pro Leu Ser Ala Ile Ala Thr Ile Ser Ala Gly Cys Trp Asp Lys
97          20          25          30
100 Glu Thr Thr Lys Glu Glu Lys Ser Ala Asp Asn Gln Asn Lys Gln Ile
101          35          40          45
104 Thr Asp Val Ser Lys Ile Ser Gly Leu Val Asn Glu Arg Lys Ser Glu
105          50          55          60
108 Ile Met Ala Ala Lys Ala Asp Ala Asn Lys His Phe Gly Leu Asn Met
109 65          70          75          80
112 Ala Ile Val Thr Ala Gly Gly Thr Val Asn Asp Asn Ser Phe Asn Gln
113          85          90          95
116 Ser Ser Trp Glu Ala Ile Gln Gln Leu Gly Ala Leu Thr Gly Gly Glu
117          100         105         110
120 Ile Thr Ser Val Asp Ser Ser Thr Ala Glu Leu Glu Gly Lys Tyr Ser
121          115         120         125
124 Ser Leu Ala Asn Thr Asn Lys Asn Val Trp Val Leu Ser Gly Phe Gln
125          130         135         140
128 His Gly Asp Ala Phe Thr Arg Trp Leu Lys Ile Pro Glu Asn Lys Gln
129 145          150         155         160
132 Leu Phe Thr Glu Lys Asn Ile Ile Ile Leu Gly Ile Asp Trp Thr Asp
133          165         170         175
136 Thr Glu Asn Val Ile Pro Thr Gly Arg Tyr Ile Asn Leu Thr Tyr Lys
137          180         185         190
140 Thr Glu Glu Ala Gly Trp Leu Ala Gly Tyr Ala Asn Ala Ser Phe Leu
141          195         200         205
144 Ala Lys Lys Phe Pro Ser Asp Pro Thr Lys Arg Ser Ala Ile Val Ile
145          210         215         220
148 Gly Gly Gly Ile Ser Pro Ala Val Thr Asp Phe Ile Ala Gly Tyr Leu
149 225          230         235         240
152 Ala Gly Ile Lys Ala Trp Asn Leu Lys Asn Ser Asp Lys Lys Thr Lys
153          245         250         255
156 Ile Thr Thr Asp Lys Ile Glu Ile Asn Leu Gly Phe Asp Val Gln Asp
157          260         265         270
160 Thr Ser Thr Lys Glu Arg Leu Glu Gln Ile Ala Ser Lys Asp Lys Pro
161          275         280         285
164 Ser Thr Leu Leu Ala Val Ala Gly Pro Leu Thr Glu Ile Phe Ser Asp
165          290         295         300
168 Ile Ile Ala Asn Gln Asn Asp Arg Tyr Leu Ile Gly Val Asp Thr Asp
169 305          310         315         320
172 Gln Ser Leu Val Tyr Thr Lys Thr Lys Asn Lys Phe Phe Thr Ser Ile
173          325         330         335
176 Leu Lys Asn Leu Gly Tyr Ser Val Phe Ser Val Leu Ser Asp Leu Tyr

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177          340          345          350
180 Thr Lys Lys Ser Asn Ser Arg Asn Leu Ala Gly Phe Glu Phe Gly Lys
181          355          360          365
184 Lys Ser Ala Thr Val Tyr Leu Gly Ile Lys Asp Arg Phe Val Asp Ile
185          370          375          380
188 Ala Asp Thr Ser Leu Glu Gly Asn Asp Lys Lys Leu Ala Thr Glu Ala
189 385          390          395          400
192 Ile Ser Glu Ala Lys Lys Glu Phe Glu Glu Lys Thr Lys Thr Ile Pro
193          405          410          415
196 Ala Glu Glu Val Arg Lys Thr Leu Glu Ile Pro Glu Met Pro Asp Lys
197          420          425          430
200 Gln Pro Asp Lys Gln Gln Glu Ser Leu Asp Lys Leu Ile Thr Asp Ile
201          435          440          445
204 Asn Lys Asn
205          450

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208 <210> SEQ ID NO: 3

209 <211> LENGTH: 1263

210 <212> TYPE: DNA

211 <213> ORGANISM: Artificial Sequence

213 <220> FEATURE:

214 <223> OTHER INFORMATION: Description of Artificial Sequence: mhp3 manipulated for in vitro

215 expression

217 <400> SEQUENCE: 3

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218 atgtgggata aagaaacaac taaagaagaa aaatcagccg ataatcaaaa taagcaaadc      60
220 actgatgtct caaaaatttc aggactagtt aatgaacgaa aatccgaaat tatggccgca      120
222 aaagctgatg caaacaaaca ttttgggcta aatatggcaa ttgtaaccgc tggggaacg      180
224 gtaaatgata attcatttaa ccaatcargt tgggaggcaa ttcaacaact tggcgctctt      240
226 actggaggtg agattacttc agtagatagt tcaactgctg aacttgaagg aaaatatagc      300
228 tcaattgcta ataccaacaa aaatgttttg gtactttctg gttttcaaca cggatgatgc      360
230 ttcacaagat gggttaaaaat ccctgaaaat aagcaattat ttactgaaaa aaatattatc      420
232 atactcggaa ttgactggac tgatactgaa aatgtaattc caacaggtcg atatattaat      480
234 ttaacctata aaactgaaga agccggatgg cttgcaggat atgcgaatgc ttcctttttg      540
236 gcaaaaaaat tcccaagtga tccaactaaa agatcagcaa ttgttatcgg tgggaggatt      600
238 tcgccagctg taactgattt tatcgctggg tatctagccg gaattaaagc ttggaatcta      660
240 aaaaattctg ataaaaaaac aaagataaca actgataaaa tcgagataaa tcttgggttt      720
242 gatgttcaag atacttcaac aaaagaaaga cttgaacaaa ttgcttcaaa agataaacct      780
244 tcaacactat tagctgtcgc tggaccactt actgaaattt tctcggatat aatcgcaaac      840
246 caaatgatc gttatctcat tgggtgtgac accgaccaat cacttgttta taaaaaaact      900
248 aaaaataaat ttttcacctc aattttgaaa aatttaggtt actccgtttt cagcgttctt      960
250 agtgatttat ataccaaaaa atcaaattca agaaatttag ccggctttga atttggtaaa     1020
252 aaaagtgcaa ccgtttatct tggaattaaa gacaggtttg tcgatattgc tgatacttct     1080
254 ttagaaggca atgataaaaa actcgcaact gaagccattt ctgaagctaa aaaagaattt     1140
256 gaagaaaaaa ctaagacaat tctgcccga gaagttcgta aaactttaga aattccggaa     1200
258 atgcctgata aacaacctga taagcaacag gaaagcttag acaaacttaa ttaccgatat     1260
260 taa                                           1263

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263 <210> SEQ ID NO: 4

264 <211> LENGTH: 423

265 <212> TYPE: PRT

266 <213> ORGANISM: Artificial Sequence

RAW SEQUENCE LISTING

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Output Set: N:\CRF4\10262004\I676249D.raw

268 <220> FEATURE:

269 <223> OTHER INFORMATION: Description of Artificial Sequence: mhp3 manipulated for in
270 vitro expression

272 <400> SEQUENCE: 4

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274 Met Trp Asp Lys Glu Thr Thr Lys Glu Glu Lys Ser Ala Asp Asn Gln
275 1 5 10 15
278 Asn Lys Gln Ile Thr Asp Val Ser Lys Ile Ser Gly Leu Val Asn Glu
279 20 25 30
282 Arg Lys Ser Glu Ile Met Ala Ala Lys Ala Asp Ala Asn Lys His Phe
283 35 40 45
286 Gly Leu Asn Met Ala Ile Val Thr Ala Gly Gly Thr Val Asn Asp Asn
287 50 55 60
290 Ser Phe Asn Gln Ser Gly Trp Glu Ala Ile Gln Gln Leu Gly Ala Leu
291 65 70 75 80
294 Thr Gly Gly Glu Ile Thr Ser Val Asp Ser Ser Thr Ala Glu Leu Glu
295 85 90 95
298 Gly Lys Tyr Ser Ser Leu Ala Asn Thr Asn Lys Asn Val Trp Val Leu
299 100 105 110
302 Ser Gly Phe Gln His Gly Asp Ala Phe Thr Arg Trp Leu Lys Ile Pro
303 115 120 125
306 Glu Asn Lys Gln Leu Phe Thr Glu Lys Asn Ile Ile Ile Leu Gly Ile
307 130 135 140
310 Asp Trp Thr Asp Thr Glu Asn Val Ile Pro Thr Gly Arg Tyr Ile Asn
311 145 150 155 160
314 Leu Thr Tyr Lys Thr Glu Glu Ala Gly Trp Leu Ala Gly Tyr Ala Asn
315 165 170 175
318 Ala Ser Phe Leu Ala Lys Lys Phe Pro Ser Asp Pro Thr Lys Arg Ser
319 180 185 190
322 Ala Ile Val Ile Gly Gly Gly Ile Ser Pro Ala Val Thr Asp Phe Ile
323 195 200 205
326 Ala Gly Tyr Leu Ala Gly Ile Lys Ala Trp Asn Leu Lys Asn Ser Asp
327 210 215 220
330 Lys Lys Thr Lys Ile Thr Thr Asp Lys Ile Glu Ile Asn Leu Gly Phe
331 225 230 235 240
334 Asp Val Gln Asp Thr Ser Thr Lys Glu Arg Leu Glu Gln Ile Ala Ser
335 245 250 255
338 Lys Asp Lys Pro Ser Thr Leu Leu Ala Val Ala Gly Pro Leu Thr Glu
339 260 265 270
342 Ile Phe Ser Asp Ile Ile Ala Asn Gln Asn Asp Arg Tyr Leu Ile Gly
343 275 280 285
346 Val Asp Thr Asp Gln Ser Leu Val Tyr Thr Lys Thr Lys Asn Lys Phe
347 290 295 300
350 Phe Thr Ser Ile Leu Lys Asn Leu Gly Tyr Ser Val Phe Ser Val Leu
351 305 310 315 320
354 Ser Asp Leu Tyr Thr Lys Lys Ser Asn Ser Arg Asn Leu Ala Gly Phe
355 325 330 335
358 Glu Phe Gly Lys Lys Ser Ala Thr Val Tyr Leu Gly Ile Lys Asp Arg
359 340 345 350
362 Phe Val Asp Ile Ala Asp Thr Ser Leu Glu Gly Asn Asp Lys Lys Leu

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363          355          360          365
366 Ala Thr Glu Ala Ile Ser Glu Ala Lys Lys Glu Phe Glu Glu Lys Thr
367          370          375          380
370 Lys Thr Ile Pro Ala Glu Glu Val Arg Lys Thr Leu Glu Ile Pro Glu
371 385          390          395          400
374 Met Pro Asp Lys Gln Pro Asp Lys Gln Gln Glu Ser Leu Asp Lys Leu
375          405          410          415
378 Ile Thr Asp Ile Asn Asn Leu
379          420
382 <210> SEQ ID NO: 5
383 <211> LENGTH: 602
384 <212> TYPE: DNA
385 <213> ORGANISM: Mycoplasma hyopneumoniae
387 <400> SEQUENCE: 5
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390 aacgcacac cgtgttgaaa accagaaagt actcaaacat tttgttggt attagcaagt      120
392 gagctatatt ttccttcaag ttcagcagtt gaactatcta ctgaagtaat ctcacctcca      180
394 gtaagagcgc caagttgttg aattgcctct caacttgatt ggtaaataga attatcattt      240
396 accgttccac cagcggttac aattgccata tttagcccaa aatgtttggt tgcacagct      300
398 tttgcgccca taatttcgga ttttcgttca ttaactagtc ctgaaatatt tgagacatca      360
400 gtgatttgct tattttgatt atcggctgat ttttcttctt tagttgtttc tttatcccaa      420
402 catccggcag agattgtcgc gattgctgaa agcggaaaaa ctaagcctaa gccagaagaa      480
404 ttatttcatt ttatcttttt tttcatagtt gttctcctaa ttaattgttt taattacgat      540
406 gactttcaat ttttttttaa taaattaatt tttattttac attttctatt atattcaaaa      600
408 ac
411 <210> SEQ ID NO: 6
412 <211> LENGTH: 200
413 <212> TYPE: PRT
414 <213> ORGANISM: Mycoplasma hyopneumoniae
416 <400> SEQUENCE: 6
418 Met Ile Ile Phe Ser Val Asn Asn Cys Leu Phe Ser Gly Ile Phe
419 1          5          10          15
422 Asn His Leu Val Asn Ala Ser Pro Cys Trp Lys Pro Glu Ser Thr Gln
423          20          25          30
426 Thr Phe Leu Leu Val Leu Ala Ser Glu Leu Tyr Phe Pro Ser Ser Ser
427          35          40          45
430 Ala Val Glu Leu Ser Thr Glu Val Ile Ser Pro Pro Val Arg Ala Pro
431          50          55          60
434 Ser Cys Trp Ile Ala Ser Gln Leu Asp Trp Leu Asn Glu Leu Ser Phe
435 65          70          75          80
438 Thr Val Pro Pro Ala Val Thr Ile Ala Ile Phe Ser Pro Lys Cys Leu
439          85          90          95
442 Phe Ala Ser Ala Phe Ala Ala Ile Ile Ser Asp Phe Arg Ser Leu Thr
443          100          105          110
446 Ser Pro Glu Ile Phe Glu Thr Ser Val Ile Cys Leu Phe Trp Leu Ser
447          115          120          125
450 Ala Asp Phe Ser Ser Leu Val Ser Leu Ser Gln His Pro Ala Glu
451          130          135          140
454 Ile Val Ala Ile Ala Glu Ser Gly Lys Thr Lys Pro Lys Pro Arg Asn

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:7; Xaa Pos. 3
Seq#:10; N Pos. 9,18,21
Seq#:12; N Pos. 6,9,12,18,21,24
Seq#:14; N Pos. 4,7,10,16,19,22

VERIFICATION SUMMARY

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Input Set : A:\3153.162.PC10555A.Second.Substitute.Seq.10.19.04.ST25.txt

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L:483 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:0
L:534 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:0
L:564 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12 after pos.:0
L:594 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14 after pos.:0